## IN THE SPECIFICATION

Please replace the paragraph beginning at page 27, line 7, with the following rewritten paragraph:

The BLAST software suite (NCBI, Bethesda MD; ~~http://www.~~ncbi.nlm.nih.gov/gorf/bl2.html), includes various sequence analysis programs including "blastn" that is used to align nucleotide sequences and BLAST2 that is used for direct pairwise comparison of either nucleotide or amino acid sequences. BLAST programs are commonly used with gap and other parameters set to default settings, e.g.: Matrix: BLOSUM62; Reward for match: 1; Penalty for mismatch: -2; Open Gap: 5 and Extension Gap: 2 penalties; Gap x drop-off: 50; Expect: 10; Word Size: 11; and Filter: on. Identity is measured over the entire length of a sequence. Brenner et al. (1998; Proc Natl Acad Sci 95:6073-6078, incorporated herein by reference) analyzed BLAST for its ability to identify structural homologs by sequence identity and found 30% identity is a reliable threshold for sequence alignments of at least 150 residues and 40%, for alignments of at least 70 residues.

Please replace the paragraph beginning at page 28, line 11, with the following rewritten paragraph:

Following assembly, templates were subjected to BLAST, motif, and other functional analyses and categorized in protein hierarchies using methods described in USSN 08/812,290 and USSN 08/811,758, both filed March 6, 1997; in USSN 08/947,845, filed October 9, 1997; and in USSN 09/034,807, filed March 4, 1998. Then templates were analyzed by translating each template in all three forward reading frames and searching each translation against the PFAM database of hidden Markov model-based protein families and domains using the HMMER software package (Washington University School of Medicine, St. Louis MO; ~~http://~~pfam.wustl.edu/). The cDNA was further analyzed using MACDNASIS PRO software (Hitachi Software Engineering), and LASERGENE software (DNASTAR) and queried against

public databases such as the GenBank rodent, mammalian, vertebrate, prokaryote, and eukaryote databases, SwissProt, BLOCKS, PRINTS, PFAM, and Prosite.

Please replace the paragraph beginning at page 9, line 27, with the following rewritten paragraph:

Mammalian variants of the cDNA encoding cancer marker protein were identified using BLAST2 with default parameters and the ZOOSEQ databases (Incyte Genomics). These preferred variants have about 90% identity to ~~the human protein~~ SEQ ID NO:2 as shown in the table below. The first column shows the SEQ $ID_H$ for the human cDNA; the second column, the SEQ $ID_{VAR}$ for variant cDNAs; the third column, the clone numbers for the variants; the fourth column, the percent identity to the human cDNA; and the fifth column, the nucleotide alignment ($Nt_H$) of the human and variant cDNAs.

| SEQ $ID_H$ | SEQ $ID_{VAR}$ | Clone No. | Identity | $Nt_H$ Alignment |
|---|---|---|---|---|
| ~~1~~ 2 | ~~9~~ | ~~702758636~~ 008031_Cf.1 | 89% | 541-1123 |
| ~~1~~ 2 | 10 | 034237_Mm.1 | 90% | 667-1173 |
| ~~1~~ 2 | 11 | 702482342 | 89% | 671-1173 |